GiPSi: A Draft Framework for Open Source/Open Architecture Software Development for Organ Simulation in the Digital Human

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Background and Problem: The field of medical and surgical simulation is currently characterized by scattered research projects using a variety of models that are neither inter-operable nor independently verifiable. The open source/open architecture software development model provides a framework to address: i) interfacing of models from multiple research groups, ii) validation of quantitative biological simulations, iii) inter-connectibility of software modules, and iv) open source or proprietary development of additional models, data, and computation modules.

Method and Tools: We propose GiPSi (General Interactive Physical Simulation Interface), an open source/open architecture framework for constructing hierarchical models of horizontally connected heterogeneous physiological processes, and developing interactive simulations of these models. GiPSi provides support for heterogeneous models of computation and defines APIs for interfacing these heterogeneous physical processes.

The models are represented as Simulation Objects. Each simulation object can be derived from a computational model contained in Modeling Tools, such as finite elements. Computational Tools, such as ODE solvers, provide a library of numerical methods for low level computation of an object's dynamics. The objects are created and maintained by the Simulation Kernel, which arbitrates their communication with other objects and components of the system. The I/O subsystem component provides user input through haptic interface tools and output through visualization tools.

Results: GiPSi has been tested on the construction of a heart model for simulation of heart surgery. This testbed model captures the important aspects of the general problem: i) multiple heterogeneous processes to be modeled and interfaced, and ii) different levels of abstraction for different processes.

Conclusion: GiPSi provides a framework that facilitates shared development to encourage extensibility and generality of the interfaces, allowing components built by different groups to plug together. Modularity is enforced through encapsulation and data hiding between components. Each model has separate geometries for visualization, simulation, and interfacing. This lets the modeler choose the most natural geometric representation for each. In addition, a standard interfacing API facilitating communication among these components is provided.

GiPSi is designed to be general and independent of the specifics of the implemented modeling methods. This allows GiPSi to seamlessly integrate heterogeneous models and processes, and enforce time dependent spatial relationships among them, which is not possible with the earlier frameworks. GiPSi is intended to be a draft specification that will be modified according to feedback we receive from the broader biological and medical simulation community at the NIH digital biology workshop.